Evaluation of Grain Yield Stability and Genetic Variation in Salt-Tolerant Bread Wheat Promising Lines and Cultivars

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ABSTRACT

Ghazvini, H., Marandi, M., and Amini Safidab, A. 2019. Evaluation of grain yield stability and genetic variation in salt-tolerant bread wheat promising lines and cultivars. **Seed and Plant Improvement Journal 35-1:** 1-24 (in Persian).

Yield stability and genetic variation in 17 salt-tolerant bread wheat promising lines and three cultivars; Arg, Bam and Ofough were evaluated in field trials as well as by molecular assay. In field, yield trials of genotypes was carried out in saline soils of Melishbar (Yazd), Amirabad (Birjand), Roudasht (Isfahan), Ekhtiarabad (Kerman) and Zahak (Zabol) agriculturar research stations, Iran, in 2012-13 and 2013-14 cropping cycle. To evaluate genetic variation among genotypes, 18 SSR markers that were previously mapped on salt-tolerant quantitative trait loci (QTLs) were used. Combined analysis of variance revealed significant differences for genotype main effect and year × location, year × genotype and year × location × genotype interaction effects. Grain yield comparison of genotypes using least significant difference(LSD) test showed that lines 14, 16, 11 and 5 with grain yields of 4.649, 4.517, 4.441 and 4.300 tha^{-1} had higher grain yields among genotypes. Different methods of stability analysis revealed that genotypes 11, 15, 16 and 20 (cultivar Ofough) had higher yield stability compared to the other genotypes. Cluster analysis of molecular data using UPGMA method and principal component analysis (PCoA) classified studied genotypes into four major groups. Results of cluster analysis based on molecular data were not in agreement with the results of field experiments. Results of Mantel's test indicated that correlation between grain yield under salinity stress conditions and their allelic diversity was about 0.13 and not-significant. Despite this weak correlation, SSR markers could greatly reveal genetic variation among wheat genotypes. This genetic variation can effectively be used in wheat breeding programs for salt tolerance in Iran.

Key words: Salinity stress, adaptation, molecular markers, cluster analysis, polymorphism information content.

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Physicochemical Attributes and Their Relationship with Organoleptic Properties of Fruits of Quince (*Cydonia oblonga* Mill.) Genotypes Collected From Different Regions of Iran

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ABSTRACT

Abdollahi, H., Alipour, M., and Mohammadi Garmaroudi, M. 2019. Physicochemical attributes and their relationship with organoleptic properties of fruits of quince (*Cydonia oblonga* Mill.) genotypes collected from different regions of Iran. **Seed and Plant Improvement Journal 35-1:** 25-46 (in Persian).

Due to several reasons such as firmness and high astringency, the fruits of quince are rarely used as table fruit, however, there are genotypes that produce fruits for table fruits. Considering this issue, in current research, the organoleptic properties and their relationship with physicochemical attributes of fruits of quince genotypes collected from different regions of Iran were evaluated in Karaj, Iran. The organoleptic properties included aroma, juiciness, sensory firmness, astringency and taste of pulp, while physical fruit firmness, pH, TSS, TA were also evaluated as physicochemical attributes. Means of physicochemical attributes were: physical fruit firmness with 12.6 kg/cm^2, TSS with 16.2 °Brix and TA equivalent to 9.8 mEq/mg titratable acids. Fruits of quince genotypes originated from Kashan region, especially KVD4, with physical fruit firmness as high as 15.3 kg/cm^2 had the firmest fruit texture. On the contrary, the fruit of genotypes originated from Guilan region, in general, had the softest fruits texture. TSS in all genotypes ranged from 14-19 °Brix, but similarly the fruits of Guilan region had the lowest TSS levels. PH2 and SVS2 genotypes had the highest TSS that could be the main reason that they gained highest sensory values in the organoleptic tests. The organoleptic tests demonstrated that sensory values were highest in the fruits of genotypes originated from Isfahan plain; in this case the highest sensory values were evaluated in fire blight susceptible genotype, KM1, followed by NB4 and Isfahan cultivar. The lowest sensory values were scored in Guilan genotypes, and AS2 genotype demonstrated the lowest scores. Fruit firmness by sensory evaluation were significantly correlated with physical firmness. Correlation analysis also showed that the total score of fruit in organoleptic tests were significantly and positively correlated with all of the organoleptic properties, except fruit astringency. It is concluded that the quince genotypes originated from Isfahan province are the most important genetic resources for selection and breeding of new quince cultivars, both for growth and bearing habit purposes as reported in the previous works as well as for fruit quality based on the results reported in this research.

Key words: Quince, sensory test, quince cv. Isfahan, table fruit, astringency.

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Evaluation of Some Characteristics of Collected Pomegranate Germplasm from Kerman Province in Iran

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ABSTRACT

Zahravi, M., and Vazifehshenas, M. R. 2019. Evaluation of some characteristics of collected pomegranate germplasm from Kerman province in Iran. **Seed and Plant Improvement Journal 35-1:** 47-71 (in Persian).

To study genetic diversity in pomegranate germplasm collected from Kerman province, 94 accessions from the pomegranate collection of the National Plant Genetic Bank of Iran in Yazd were evaluated. For this purpose, 21 qualitative attributes were evaluated using the international descriptor for pomegranate. Analysis of Shannon index showed that shape of fruit base, seed color and vigour of tree had the highest, and color of one-year-old shoot, growth habit and bearing habit had the lowest diversity. Variation of Shannon index in each type of sweet, sweet-sour and sour genotypes followed similar pattern. Dendorgram of the cluster analysis divided sweet, sweet-sour and sour genotypes into five, seven, and eight groups, respectively. The results of boxplot study based on genotype origins indicated higher variation in the genetic distances of Ravar, Baft and Rafsanjan areas with other regions. The origins of the genotypes were divided into five groups using dendrogram. Ravar, Rafsanjan and Baft formed one group. Jiroft and Shahdad also belonged to a common group, and Sharababak and Bam, in a separate group. Sirjan and Chatroud regions stood individually in dendrogram. Results of cluster analysis by K-means method, using the principal components, showed that based on the Bayesian information criterion (BIC), the maximum genetic differentiation obtained at K = 10. The characteristics of each of the ten groups were studied. The results of this research in the field of genetic differentiation and germplasm grouping will be useful in future studies to identify genotypes and to select accssions with high levels of differentiation.

Key words: Pomegranate, gene bank, genetic diversity, genetic variation, gene pool.

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Evaluation of Vegeteative and Pomological Characteristics and Fruit Yield of Some Asian Pear Cultivars under Urmia Climatic Conditions

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ABSTRACT

Hanareh, M., and Hassani, Gh. 2019. Evaluation of vegeteative and pomological characteristics and fruit yield of some Asian pear cultivars under urmia climatic conditions. **Seed and Plant Improvement Journal 35-1:** 73-94 (in Persian).

Asian pears (*Pyrus serotina* Rehd.) are different from European pears in shape, size, color, flavor, texture and ripening time of fruit. This research was conducted to study growth and fruit yield of eight Asian pear cultivars; KS6, KS7, KS8, KS9, KS10, KS12, KS13 and KS14 as well as cv. Shah Miveh and cv. Spadona as control cultivars in Kahriz field station, Urmia, Iran, from 2008 to 2015. Combined analysis of variance revealed significant differences ($P \leq 0.01$) among cultivars for vegetative characteristics including annual growth, tree height, trunk diameter and tree canopy, and fruit attributes; fruit length, diameter, weight, firmness, TSS, pH and TA, fruits number per tree, fruit yield per tree, and fruit yield per unit trunk cross-sectional area (TCSA) index. The lowest vegetative growth was observed in KS14 cultivar. Asian cultivars had fruit weight and TSS less, and fruit firmness, fruit number per tree, fruit yield per tree and fruit yield per unit trunk cross-sectional area greater than control cultivars. Cv. Shah Miveh with 3.73 kg and KS13 with 10.06 kg had the lowest and the highest mean fruit yield per tree for last three years. The highest yield per unit trunk cross-sectional area index was observed in KS13. Among Asian pear cultivars; KS7, KS10, as early ripening, and KS13, KS13, as medium ripening with high fruit yield and marketability can be recommened for being grown in Urmia and other regions with similar climatic conditions.

Key words: Asian pear, tree height, trunk diameter, fruit quality, fruit yield index.

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Evaluation of Resistance Level of Some Selected Local Apple Genotypes to Fire Blight Disease

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ABSTRACT

Keshavarzi, M., Damyar, S., Atashkar, D., and Naderpour, M. 2019. Evaluation of resistance level of some selected local apple genotypes to fire blight disease. **Seed and Plant Improvement Journal 35-1:** 95-108 (in Persian).

Fire blight disease caused by *Erwinia amylovora* is one of the most important diseases of pome fruits worldwide. In this research, the resistance of 24 selected apple genotypes was evaluated using a mixture of four *Erwinia amylovora* strains collected from Alborz, Kordestan, West Azarbijan and Khorassan Razavi. The plant material was grafted on apple seedlings in 2013. The grafted plants were transferred to the greenhouse and evaluated for fire blight resistance in spring 2015 and 2016- using shoot-tip inoculation method. Five weeks after inoculation, the blight severity were scored and recorded based on the progression of necrotic area on shoots. Based on the results, the fire blight severity was higher in 2015 than 2016 (24.54% and 17.68%, respectively). The results also indicated that seedling (SSB) and Shemirani Tabestaneh (SH2) genotypes were susceptible and three genotypes including Bigi Kenar Roundkhameh (B-K-Kh), Torbati (T-R1) and Kouzehei Salmasi (Go-Sa) were resistant. Genotypes were grouped into four classes including; susceptible (4.35%), moderately susceptible (13.04%), moderately resistant (17.39%) and resistant (65.52%), and there was no highly susceptible genotype. The results showed that most of the local apple genotypes examined in this research were resistant to fibre blight disease.

Key words: Apple, pome fruit, susceptibility, inoculum, necrosis.

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Evaluation of Relative Resistance of Some Walnut Commercial Cultivars and Promising Genotypes to Shallow Bark Canker (*Brenneria nigrifluens*)

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ABSTRACT

Soleymani, N., Keshavarz, M., HassanZadeh, N., Hasani, N. and Soleymani, A. 2019. Evaluation of relative resistance of some walnut commercial cultivars and promising genotypes to shallow bark canker (*Brenneria nigrifluens*). **Seed and Plant Improvement Journal 35-1:** 109-120 (in Persian).

Shallow bark canker caused by *Brenneria nigrifluens* is an important walnut disease which causes reduction in yelid and wood quality, tree decline and death. In this research, relative resistance of four local walnut genotypes KZ3, 88-1, H2-12, H2-1, one improved cv. Jamal, and eight commercial introduced cultivars; Lara, Serr, Pedro, Vina, Shinova, Chandler, RDM and Hartley (susceptible control) to brack canker and its relationship with the inoculated organs were evaluated. Disease samples were collected from Kohgiloyeh and Boyrahmad province and causal bacterial strains isolated and identified using common phenotypic tests. A mixed suspension from four selected strains was used as inoculum. Plant materials were grafted in winter 2012 and inoculated in spring 2015 in orchard conditions and canker length was measured 18 months later in winter 2016. The canker causal agent was identified as *Brenneria nigrifluens*. Canker severity was different among walnut genotypes and cultivars, Hartley and Shinova with average canker length at four centimeters and 1.75 cm were rated as the most susceptible and resistant, respectively. No cultivar or genotype was completely resistant. Both shoot and trunk were susceptible, but trunk with mean canker length of 2.91 cm was more susceptible than shoot with 1.90 cm mean canker length. A significant positive correlation was found between organ diameter and canker length ($r = 0.56^{**}$). Walnut cultivars and genotypes demonstrated different levels of resistance to shallow bark canker. Considering adverse effects of drought on canker severity and prevailing drought conditions in Iran, identification and growing walnut cultivars with relative resistance to this disease can reduce economic losses.

Key words: Walnut, inoculum, canker length, shoot, trunk.

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